AMENDMENTS TO THE CLAIMS

The following listing of the claims replaces all prior versions and listings of the claims for this application. Within this listing of the claims, the following changes have been made: claims 1, 20, 21, 28, 33, and 38 have been amended; claims 2-5, 25, and 26 have been canceled; and claims 115 to 118 are new. Claims 40-114 were previously canceled in response to a restriction requirement election. Deleted subject matter is identified by either double brackets or a strikethrough and added subject matter is underlined in bold.

LISTING OF THE CLAIMS:

1. **(Currently Amended)** A method of employing oligonucleotide probes to obtain information on a target nucleic acid analyte containing a target sequence segment, the method comprising:

contacting the analyte, under hybridizing conditions, with at least two oligonucleotide probes **[[,]]** ~~each oligonucleotide probe comprising a sequence segment complementary to the target sequence or complementary to the target sequence except at a position of interest~~ **that have at least one overlapping nucleotide in common and at least one variable nucleotide,**

~~wherein each of the at least two oligonucleotide probes has one nucleotide capable of base pairing with one nucleotide of at least two sets of two or more nucleotides, said sets having one nucleotide in common and lacking one nucleotide present in the target sequence segment; and~~

~~wherein hybridization of each oligonucleotide probe to the target sequence segment under the hybridizing conditions occurs only if no mismatch exists at the position of interest, such that depending upon the identity of the nucleotide at the position of interest, all, some or none of the at least two oligonucleotide probes hybridize to the target sequence segment~~

wherein hybridization of the at least two oligonucleotide probes to the target sequence segment occurs only if the at least one variable nucleotide of the at least two oligonucleotide probes base pairs with a corresponding nucleotide on the target sequence segment.

2-5. **(Canceled)**

6. **(Previously presented)** The method of claim 1 used for sequencing the target nucleic acid analyte.

7. **(Previously presented)** The method of claim 6 further comprising an array of oligonucleotide probes, wherein the sequence of the target nucleic acid analyte is determined by analysis of hybridization data obtained from the array of oligonucleotide probes.

8. **(Original)** The method of claim 7 wherein the array comprises arrayed individual beads or particles, each bead or particle having a surface to which is attached a plurality of oligonucleotide probes of identical sequence.

9. **(Original)** The method of claim 7 wherein the array comprises a substrate having a surface, the surface having a plurality of discrete surface sites, each site having attached a plurality of oligonucleotide probes of identical sequence.

10. **(Previously presented)** The method of claim 7 wherein the target sequence segment hybridized to the oligonucleotide probe is detected by a discrete label moiety linked to the target sequence segment.

11. **(Original)** The method of claim 10 wherein the discrete label moiety linked to the target sequence segment comprises a nucleic acid sequence.

12. **(Original)** The method of claim 10 wherein the discrete label moiety linked to the target sequence segment comprises a luminescent moiety.

13. **(Original)** The method of claim 12 wherein the luminescent moiety is a chemiluminescent or fluorescent moiety.

14. **(Previously presented)** The method of claim 9 wherein the target sequence segment is detected by a target signal.

15. **(Previously presented)** The method of claim 14 wherein the target signal is ^{32}P.

16. **(Original)** The method of claim 7 wherein detection of a target sequence segment hybridizing to an oligonucleotide probe is by detection of the heat of hybridization.

17. **(Previously presented)** The method of claim 6 wherein the sequencing method is by detection of labels that attach by hybridization to the target sequence segment.

18. **(Previously presented)** The method of claim 1 wherein hybridized target nucleic acids are amplified by a polymerase enzyme.

19. **(Previously presented)** The method of claim 18 wherein the hybridized target nucleic acids are amplified by polymerase chain reaction.

20. **(Currently amended)** The method of claim 18 wherein **the** hybridized nucleic acids are amplified by an RNA replicase enzyme.

21. **(Currently amended)** The method of claim 19 **used** for genetic analysis.

22. **(Previously presented)** The method of claim 1 used for allelic analysis.

23. **(Previously presented)** The method of claim 1 wherein the target nucleic acid analyte is derived from genomic DNA.

24. **(Previously presented)** The method of claim 1 wherein the target nucleic acid analyte is derived from a cDNA.

25-26. **(Canceled)**

27. **(Original)** The method of 6 wherein the sequencing method is by analysis of hybridization data obtained from an array of target nucleic acid analyte sequences attached to a substrate surface.

28. **(Currently amended)** The method of 14 wherein the array ~~comprises arrayed~~ **is comprised of** individual beads or particles, each bead or particle having a surface**[[,]]** ~~the surface having~~ **to which are** attached a plurality of **identical** target nucleic acid analyte sequences ~~having an identical sequence~~.

29. **(Original)** The method of 14 wherein the array comprises arrayed discrete sites on a substrate surface of an integrated substrate, each site having a surface, the surface having attached a plurality of target nucleic acid analyte sequences having an identical sequence.

30. **(Original)** The method of claim 14 wherein each oligonucleotide probe sequence additionally comprises a linker moiety and a label moiety.

31. **(Previously presented)** The method of claim 30 wherein the linker moiety comprises a common nucleic acid sequence and the label moiety comprises a signature nucleic acid sequence that identifies the target sequence segment.

32. **(Original)** The method of claim 16 wherein the common nucleic acid sequence is double stranded.

33. **(Currently amended)** The method of claim **[[7]] 30** wherein the array is imaged with decoder labels comprising a nucleic aid sequence complementary to the signature sequence and a second label moiety.

34. **(Previously presented)** The method of claim 33 wherein the second label moiety comprises a luminescent moiety.

35. **(Original)** The method of claim 34 wherein the luminescent moiety is a fluorescent or chemiluminescent moiety.

36. **(Original)** The method of claim 14 wherein the substrate surface is functionalized with a surface modification to enhance hybridization.

37. **(Previously presented)** The method of claim 36 wherein the hybridization is enhanced by increasing hybridization stringency.

38. **(Currently amended)** The method of claim **[[39]] 29** wherein the electric potential at the substrate surface is electronically controlled to enhance hybridization.

39. **(Original)** The method of claim 29 wherein the integrated substrate comprises a semiconductor chip comprising electronic circuitry, wherein the electric potential at the individual array sites of the substrate surface is independently electronically controlled to enhance of hybridization.

40-114. **(Canceled).**

115. **(New)** The method of claim 1 wherein the variable nucleotide of at least one of the at least two oligonucleotide probes is a degenerately pairing nucleotide analog.

116. **(New)** The method of claim 115 wherein the degenerately pairing nucleotide analog is selected from the group consisting of dPTP and 8-oxo-dGTP.

117. **(New)** The method of claim 1 wherein the target nucleic acid analyte is DNA and the variable nucleotide of the at least two oligonucleotide probes is independently selected from the group consisting of A, T, C, and G.

118. **(New)** The method of claim 1 wherein the target nucleic acid analyte is RNA and the variable nucleotide of the at least two oligonucleotide probes is independently selected from the group consisting of A, U, C, or G.